

# SEQUENCE LISTING

jc971 U.S. PTO  
09/813214  
03/20/01

## (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: TUCKER, KENNETH  
PLOSILA, LAURA
- (ii) TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE  
PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 19
- 10 (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: PENNIE & EDMONDS  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: USA  
(F) ZIP: 10036-2711
- 15 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- 20 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Baldwin, Geraldine F.  
(B) REGISTRATION NUMBER: 31,232  
(C) REFERENCE/DOCKET NUMBER: 7969-060
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (212) 790-9090  
(B) TELEFAX: (212) 869-8864  
(C) TELEX: 66141 PENNIE
- 25 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown
- 30 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- 35 Ile Gly Ile Ser Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg  
1 5 10 15  
Gly Asp Lys Ser Ile Ala Ile Gly Asp Ile Ala Gln Ala Leu Gly Ser  
20 25 30

Gln Ser Ile Ala Ile Gly Asp Asn Lys Ile Val  
35 40

(2) INFORMATION FOR SEQ ID NO:2:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Thr Val Leu Gly Gly Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "probe"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGNACNGTNC TGGGNGGNAA RAAR

24

(2) INFORMATION FOR SEQ ID NO:4:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

30 (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAA GCG GAC GGG GGG AAA GGC GGA GCC AAT GCG CGC GGT GAT AAA TCC  
Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser  
35 1 5 10 15

48

ATT GCT ATT GGT GAC ATT GCG CAA  
Ile Ala Ile Gly Asp Ile Ala Gln  
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72

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser  
1 5 10 15

Ile Ala Ile Gly Asp Ile Ala Gln  
20

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

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- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "probe"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20 YTTYTTNCCN CCNAGNACNG TNCC

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

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- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = ""probe""

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30

GGNACNGTNT TRGGNGGNAA RAAR

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

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- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = ""probe""

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 YTTYTTNCCN CCYAANACNG TNCC

24

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9542 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|    |  |      |
|----|--|------|
|    | CTATTGACTT AAATCACCAT ATGGTTATAA TTTAGCATAA TGGTAGGCTT TTTGTAAAAA  | 60   |
|    | TCACATCGCA ATATTGTTTT ACTGTTACTA CCATGCTTGA ATGACGATCC AAATCACCAG  | 120  |
| 15 | ATTCATTCAA GTGATGTGTT TGTATACGCA CCATTTACCC TAATTATTTT AATCAAATGC  | 180  |
|    | CTATGTCAGC ATGTATCATT TTTAAGGTA AACCACCATG AATCACATCT ATAAAGTCAT   | 240  |
|    | CTTTAACAAA GCCACAGGCA CATTTATGGC CGTGGCGGAA TATGCCAAAT CCCACAGCAC  | 300  |
|    | GGGGGGGGGT AGCTGTGCTA CAGGGCAAGT TGGCAGTGTA CGCACTCTGA GCTTTGCCCCG | 360  |
| 20 | TATTGCCGCG CTCGCTGTCC TCGTGATCGG TGCACGCTC AATGGCAGTG CTTATGCAGG   | 420  |
|    | TATCGGAATT AGTGAAGCAG ACGGGGGAAA AGGCGGAGCC AATGCGCGCG GTGATAAATC  | 480  |
|    | CATTGCTATT GGTGATATTG CTCAGGCACT TGGCTCTCAA TCTATTGCTA TCGGTGACAA  | 540  |
|    | CAAAATAGTT CATAATTCAA ATAATAATGC TAATATAGGT GCCAAAGCCT CAGGTAATGA  | 600  |
|    | GTCCATCGCC ATCGGTGGTG ATGTATTGGC TTCTGGTCAT GCCTCGATTG CCATCGGTAG  | 660  |
| 25 | TGATGACTTA TATTTGAAAA AGGAAACGGT ACAGCAAATC TCAGAGCTTC TACCTATTAT  | 720  |
|    | TCGCGGACAG AAAGCATTAA ACGATATATA CCAACTAGCT GACACTAATC TTCAAAAATA  | 780  |
|    | TAGACGCACA CACGCACAGG GACACGCCAG TACTGCAGTG GGAGCCATGT CATATGCAAA  | 840  |
|    | GGGTCATTTT TCCAACGCCT TTGGTACACG GGCAACAGCT GAAGGTACCT ATTCCTTGGC  | 900  |
| 30 | AGTGGGTCTT ACCGCCACAG CCAAAGCAGC ATCTTCAATC GCTGTTGGTT CTAATGCACA  | 960  |
|    | AGCTATCGGG TTTGCAGCGA CAGCCGTTGG TGGAAGTACT CAAGTTAATT TGAATCGAGG  | 1020 |
|    | TATTGCCCTA GGTTTTGGTT CTCAGGTCCT TCAGAAGGAT AATGATGTAA ATGCAGCAAA  | 1080 |
|    | TGTACGGGCC TATGCACCAG ATGATAACCA GCCAATAGAC AACCGGTATA AAGCCACCTT  | 1140 |
|    | CAAGAATGGT GCTACGGATG TATTTTCCAT TGTAATAGT AATGGGAATG ACAGTATCAG   | 1200 |
| 35 | GCGTAAATC ATCAATGTCG GTGCAGGTTT TCGGATACC GATGCGGTCA ATGTGGCACA    | 1260 |
|    | GCTTAAAGAG GCGGTGAGGC TGGCTAATCG TCAAATTACT TTTAAGGGTG ATGATAGCAA  | 1320 |

|    |             |            |            |             |             |            |      |
|----|-------------|------------|------------|-------------|-------------|------------|------|
|    | TAATAGAGTA  | GAAAAAGGTT | TGGGCAAGAC | TTTAACTATC  | ACAGGTGGTG  | CACAGACCAG | 1380 |
|    | CGCATTAAACC | GATCATAACA | TCGGTGTGGT | ACAAAATGGC  | GATGGTCTGA  | AAGTTCAACT | 1440 |
|    | TGCTGAAACT  | TTAACCAGCC | TTAAAATGGT | TACCACTGAA  | AACCTAACCG  | CCAACGAGAA | 1500 |
|    | AGTTACCGTA  | GGCAAAACCC | GCCTTACCAC | AGATAAAATT  | GGTTTTACCA  | ATGATATGAA | 1560 |
| 5  | TGGCATTGAT  | GAAAGCAAAC | CTTATCTTGA | TAAAGACACT  | GGCATTTCATG | CAGGTGGTCA | 1620 |
|    | AAAGATTACC  | AAACTTACTG | CTGGTGTAGT | AGATGACGAT  | GCGGCAACTT  | ATGGACAGCT | 1680 |
|    | TAAAAAAGTT  | AACCAAACCG | CTGAAAGTGC | TCTACAAACC  | TTTACCGTTA  | AAAAGGTAGA | 1740 |
|    | TAAAAATGGT  | AATGATGCTA | ATGACAGCAA | AATCATCACC  | GTGGGTAAAA  | ATAACAAACC | 1800 |
| 10 | AGACGGTACT  | CAAGTCAACA | CCCTAAAACT | CAAAGGTGAA  | AACGGTGTTG  | ATGTTACAAC | 1860 |
|    | CGAAACAAAT  | GGTACAGTTA | CCTTTGGGCT | TAACCAAAT   | AACGGTCTGA  | CCGTTGGCAA | 1920 |
|    | CAGCACCCCTA | AACAACGATG | GCTTATCTGT | TAAAAACACC  | AATAGTAACA  | AACAAATCCA | 1980 |
|    | AGTCGGTGCT  | GATGGCATT  | CATTTACTGA | TATCAGCAAT  | AGTAAGCCAG  | GTGCTGGCAT | 2040 |
|    | TGAAAATACC  | ACTCGCATT  | CCAGAGACGG | TATTGGTTTT  | GCTAATAATA  | CTGGTTCATT | 2100 |
| 15 | GGATGCAAAC  | AAACCCCGCC | TAACCCCAAC | TGGCATTAAAC | GCAGGTGGTA  | AAGAGCTGAC | 2160 |
|    | CAATGTCCAA  | TCTGCCATTA | ACCCTGCTAC | CAATGGTGGG  | CAGCTAGACT  | TTATGAACCG | 2220 |
|    | CCTAAGCACT  | GCTAATACCG | AAAAATCAGG | CTCTGCCGCC  | ACCATTAAAG  | ACTTATACAA | 2280 |
|    | CCTATCACAA  | GTACCGCTGA | CCTTTGCAGG | TGATACAGGT  | CCTAATGTCA  | CCAAAAAACT | 2340 |
| 20 | GGGCGAGATT  | TTAAAGGTTA | AAGGTGGTAA | AACCACAGCT  | GATGATTTAA  | CCAAAAATAA | 2400 |
|    | CATCGGTGTG  | GTGGCTGATA | GTACCGATAA | TAGCTTAACC  | GTTAAACTTG  | CTAAAACTTT | 2460 |
|    | AAGCGATCTT  | GATGCGGTTA | ATACTAAAAC | CCTAACTGCC  | AGCGATAAAG  | TTACCGTAGA | 2520 |
|    | CAGTGGAAC   | AACACCGCTA | AGCTACAAAA | TGGTGATTTA  | ACCTTTAGCA  | AACAAAATAC | 2580 |
|    | AGGTGCTACC  | CCTGCCACCA | ACAGCAAAAC | CATCTATGGC  | GTTGATGGCT  | TGAAGTTTAC | 2640 |
| 25 | TGATAACAAT  | GGTATAGCAC | TTGACGGCAC | AACTTACATC  | ACCAAAGACA  | AAGTTGGCTT | 2700 |
|    | TGCTAAGCAA  | GATGGTTCAC | TTGATAAAAG | CAAACCTTAT  | CTTGATAAGG  | ACAAGCTAAA | 2760 |
|    | AGTGGGTGAA  | GTTGAGATTA | CCACCAACGG | CATTAATGCA  | GGTGGTAAAG  | CCATCACAGG | 2820 |
|    | ACTAAGCAAT  | ACCCTAACCG | ATGCCACCAA | CGCAACAACA  | GGGCATGTAA  | CTCAATTGGG | 2880 |
| 30 | TATCGTTGAT  | AGTACTGACA | AAACCCGTGC | CGCCAGCATT  | GGTGATGTGC  | TAAACGCAGG | 2940 |
|    | CTTTAACCTA  | AAAAATAATG | GTGACGCCAA | AGACTTTGTC  | TCCACTTATG  | ACACTGTTGA | 3000 |
|    | TTTTATCAAT  | GGCAATGCCA | CCACCGCTAA | AGTCACTTAT  | GATGGCAAAG  | CCAGTAAAGT | 3060 |
|    | GGCGTATGAT  | GTCAATGTGG | ATGGTACAAC | CATTCATCTA  | ACAGGCGCTG  | ATGGCAATAA | 3120 |
|    | AAACCAAATT  | GGCGTAAAAA | CCACCACACT | GACCAAAACA  | GATGCTAAAG  | GTGATAAAGC | 3180 |
| 35 | AATTAACTTT  | AGTGTTAACT | CTGGTGATGA | CAAAGCCCTT  | ATTAACGCCA  | AAGACATCGC | 3240 |
|    | CGACAATCTA  | AACACCCTAG | CTGGTGAAAT | TCGCAACACC  | AAAGGCACAG  | CAGACACCGC | 3300 |

|    |            |            |            |            |            |             |      |
|----|------------|------------|------------|------------|------------|-------------|------|
|    | CCTACAAACC | TTTCAAGTCA | AAAAAGTCAA | AGAAAATGGT | GATGATGATA | ATGACGCTGA  | 3360 |
|    | CACCATCACC | GTGGGTAAAG | ATGCAAAAAC | CAATCAAGTC | AACACCCTAA | AACTCAAAGG  | 3420 |
|    | TAAAAACGGT | CTTGATATTC | AAACCAATAA | AGATGGTACG | GTTACCTTTG | GCATTAACAC  | 3480 |
|    | CCAAAGCGGT | CTTAAAGCCG | GCAACAACAC | CACTCTAAAC | AACAATGGCT | TGTCTATTAA  | 3540 |
| 5  | AAACACCGCT | GGTAACGAAC | AAATCCAAGT | CGGTGCTGAT | GGCGTGAAGT | TTGCCAAGGT  | 3600 |
|    | TAATAATGGT | GTTGTAGGTG | CTGGCATTGA | TGGCACAAC  | CGCATTACCA | GAGATGAAAT  | 3660 |
|    | TGGCTTTGCT | GGGACTAATG | GCTCACTTGA | TAAAAGCAAA | CCCCACCTAA | GCAAAGACGG  | 3720 |
|    | CATTAACGCA | GGTGGTAAAA | AGATTACCAA | CATTCAATCA | GGTGAGATTG | CCCAAAACAG  | 3780 |
| 10 | CAATGATGCT | GTGACAGGCG | GCAAGATTTA | TGATTTAAAA | ACCGAACTTG | AAAACAAAAT  | 3840 |
|    | CAGCAGTACT | GCCAAAACAG | CACAAAAC   | TTCTCAGTAG | CAGATGAACA |             | 3900 |
|    | AGGTAATAAC | TTTACGGTTA | GTAACCTTA  | CTCCAGTTAT | GACACCTCAA | AGACCTCTGA  | 3960 |
|    | TGTCATCACC | TTTGCAGGTG | AAAACGGCAT | TACCACCAAG | GTAATAAAG  | GTGTGGTGCG  | 4020 |
|    | TGTGGGCATT | GACCAAACCA | AAGGCTTAAC | CACGCCTAAG | CTGACCGTGG | GTAATAATAA  | 4080 |
| 15 | TGGCAAAGGC | ATTGTCATTG | ACAGCCAAAA | TGGTCAAAAT | ACCATCACAG | GACTAAGCAA  | 4140 |
|    | CACTCTAGCT | AATGTTACCA | ATGATAAAG  | TAGCGTACGC | ACCACAGAAC | AGGGCAAGAT  | 4200 |
|    | AATCAAAGAC | GAAGACAAAA | CCCGTGCCGC | CAGCATTGTT | GATGTGCTAA | GCGCAGGCTT  | 4260 |
|    | TAAGTTGCAA | GGCAATGGTG | AAGCGGTTGA | CTTTGTCTCC | ACTTATGACA | CTGTCAACTT  | 4320 |
| 20 | TGCCGATGGC | AATGCCACCA | CCGCTAAGGT | GACCTATGAT | GACACAAGCA | AAACCAGTAA  | 4380 |
|    | AGTGGTCTAT | GATGTCAATG | TGGATGATAC | AACCATTGAA | GTAAAGATA  | AAAAACTTGG  | 4440 |
|    | CGTAAAAACC | ACCACATTGA | CCAGTACTGG | CACAGGTGCT | AATAAATTTG | CCCTAAGCAA  | 4500 |
|    | TCAAGCTACT | GGCGATGCGC | TTGTCAAGGC | CAGTGATATC | GTTGCTCATC | TAAACACCTT  | 4560 |
|    | ATCTGGCGAC | ATCCAAACTG | CCAAAGGGGC | AAGCCAAGCG | AACAGCTCAG | CAGGCTATGT  | 4620 |
| 25 | GGATGCTGAT | GGCAATAAGG | TCATCTATGA | CAGTACCGAT | AACAAGTACT | ATCAAGCCAA  | 4680 |
|    | AAATGATGGC | ACAGTTGATA | AAACCAAAGA | AGTTGCCAAA | GACAAACTGG | TCGCCCCAAGC | 4740 |
|    | CCAAACCCCA | GATGGCACAT | TGGCTCAAAT | GAATGTCAAA | TCAGTCATTA | ACAAAGAACA  | 4800 |
|    | AGTAAATGAT | GCCAATAAAA | AGCAAGGCAT | CAATGAAGAC | AACGCCTTTG | TTAAAGGACT  | 4860 |
| 30 | TGAAAAAGCC | GCTTCTGATA | ACAAAACCAA | AAACGCCGCA | GTAAGTGTGG | GTGATTTAAA  | 4920 |
|    | TGCCGTTGCC | CAAACACCGC | TGACCTTTGC | AGGGGATACA | GGCACAACGG | CTAAAAAACT  | 4980 |
|    | GGGCGAGACT | TTGACCATCA | AAGGTGGGCA | AACAGACACC | AATAAGCTAA | CCGATAATAA  | 5040 |
|    | CATCGGTGTG | GTAGCAGGTA | CTGATGGCTT | CACTGTCAAA | CTTGCCAAAG | ACCTAACCAA  | 5100 |
|    | TCTTAACAGC | GTTAATGCAG | GTGGTACCAA | AATTGATGAC | AAAGGCGTGT | CTTTTGTAGA  | 5160 |
| 35 | CTCAAGCGGT | CAAGCCAAAG | CAAACACCCC | TGTGCTAAGT | GCCAATGGGC | TGGACCTGGG  | 5220 |
|    | TGGCAAGGTC | ATCAGCAATG | TGGGCAAAGG | CACAAAAGAC | ACCGACGCTG | CCAATGTACA  | 5280 |

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|----|--|------|
|    | ACAGTTAAAC GAAGTACGCA ACTTGTTGGG TCTTGGAAT GCTGGTAATG ATAACGCTGA   | 5340 |
|    | CGGCAATCAG GTAAACATTG CCGACATCAA AAAAGACCCA AATTCAGGTT CATCATCTAA  | 5400 |
|    | CCGCACTGTC ATCAAAGCAG GCACGGTACT TGGCGGTAAA GGTAATAACG ATACCGAAAA  | 5460 |
|    | ACTTGCCACT GGTGGTGTAC AAGTGGGCGT GGATAAAGAC GGCAACGCTA ACGGCGATTT  | 5520 |
| 5  | AAGCAATGTT TGGGTCAAAA CCCAAAAAGA TGGCAGCAAA AAAGCCCTGC TCGCCACTTA  | 5580 |
|    | TAACGCCGCA GGTCAGACCA ACTATTTGAC CAACAACCCC GCAGAAGCCA TTGACAGAAT  | 5640 |
|    | AAATGAACAA GGTATCCGCT TCTTCCATGT CAACGATGGC AATCAAGAGC CTGTGGTACA  | 5700 |
|    | AGGGCGTAAC GGCATTGACT CAAGTGCCTC AGGCAAGCAC TCAGTGGCGA TAGGTTTCCA  | 5760 |
| 10 | GGCCAAGGCA GATGGTGAAG CCGCCGTTGC CATAGGCAGA CAAACCCAAG CAGGCAACCA  | 5820 |
|    | ATCCATCGCC ATCGGTGATA ACGCACAAGC CACAGGCGAT CAATCCATCG CCATCGGTAC  | 5880 |
|    | AGGCAATGTG GTAGCAGGTA AGCACTCTGG TGCCATCGGC GACCCAAGCA CTGTTAAGGC  | 5940 |
|    | TGATAACAGT TACAGTGTGG GTAATAACAA CCAGTTTACC GATGCCACTC AAACCGATGT  | 6000 |
|    | CTTTGGTGTG GGCAATAACA TCACCGTGAC CGAAAGTAAC TCGGTTGCCT TAGGTTCAAA  | 6060 |
| 15 | CTCTGCCATC AGTGCAGGCA CACACGCAGG CACACAAGCC AAAAAATCTG ACGGCACAGC  | 6120 |
|    | AGGTACAACC ACCACAGCAG GTGCAACCGG TACGGTTAAA GGCTTTGCTG GACAAACGGC  | 6180 |
|    | GGTTGGTGGC GTCTCCGTGG GTGCCTCAGG TGCTGAACGC CGTATCCAAA ATGTGGCAGC  | 6240 |
|    | AGGTGAGGTC AGTGCCACCA GCACCGATGC GGTCAATGGT AGCCAGTTGT ACAAAGCCAC  | 6300 |
| 20 | CCAAGGCATT GCCAACGCAA CCAATGAGCT TGACCATCGT ATCCACCAA ACGAAAATAA   | 6360 |
|    | AGCCAATGCA GGGATTTTCAT CAGCGATGGC GATGGCGTCC ATGCCACAAG CCTACATTCC | 6420 |
|    | TGGCAGATCC ATGGTTACCG GGGGTATTGC CACCACAAC GGTCAAGGTG CGGTGGCAGT   | 6480 |
|    | GGGACTGTCTG AAGCTGTCTG ATAATGGTCA ATGGGTATTT AAAATCAATG GTTCAGCCGA | 6540 |
|    | TACCCAAGGC CATGTAGGGG CGGCAGTTGG TGCAGTTTTT CACTTTTAAG CCATAAATCG  | 6600 |
| 25 | CAAGATTTTA CTTAAAAATC AATCTCACCA TAGTTGTATA AAACAGCATC AGCATCAGTC  | 6660 |
|    | ATATTACTGA TGCTGATGTT TTTTATCACT TAAACCATTT TACCGCTCAA GTGATTATCT  | 6720 |
|    | TTCAACATGA CCAAATCGCC ATTGATCATA GGTAAACTTA TTGAGTAAAT TTTATCAATG  | 6780 |
|    | TAGTTGTTAG ATATGGTTAA AATTGTGCCA TTGACCAAAA AATTACCGAT TTATCCCGAA  | 6840 |
| 30 | AATTTCTGAT TATGATCACT TTTCATAAAT TTCCCAATT TGTCTTTATA AATATCCCAA   | 6900 |
|    | GAAATGGTAT TATTTTATTG CCATCAGCAT ATGCGACAAC TCATCGTATC ATCTTTTTAT  | 6960 |
|    | CATAAAAATG CAAATAGGCA TATGCATTTT TTGAATTGAA CTTACGCACT GAGAGATCCC  | 7020 |
|    | CTCATAATTT CCCCAAAGCG TAACCATGTG TGAATAAATT TTGAGCTAGT AGGGTTGCAG  | 7080 |
|    | CCACGAGTAA GTCTTCCCTT GTTATTGTGT AGCCAGAATG CCGCAAACT TCCATGCCTA   | 7140 |
| 35 | AGCGAACTGT TGAGAGTACG TTTGATTTT TGACTGTGTT AGCCTGGAAG TGCTTGTCCT   | 7200 |
|    | AACCTTGTTT CTGAGCATGA ACGCCCGCAA GCCAACATGT TAGTTGAAGC ATCAGGGCGA  | 7260 |

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|----|--|------|
|    | TTAGCAGCAT GATATCAAAA CGCTCTGAGC TGCTCGTTCG GCTATGGCGT AGGCCTAGTC  | 7320 |
|    | CGTAGGCAGG ACTTTTCAAG TCTCGGAAGG TTTCTTCAAT CTGCATTTCG CTTCAATAGA  | 7380 |
|    | TATTAACAAG TTGTTTGGGT GTTCGAATTT CAACAGGTAA GTTAGTTGCT AGAATCCATG  | 7440 |
|    | GCTCCTTTGC CGACGCTGAG TAGATTTTAG GTGACGGGTG GTGACAATGA GTCCGTGTCTG | 7500 |
| 5  | AGCGCTGATT TTTTCGGCCT TTAGAGCGAG ATTTATACAA TAGAATTTGG CATGAGATTG  | 7560 |
|    | GATTGCTTTT AGTCAGCCTC TTATAGCCTA AAGTCTTTGA GTGACTAGAT GACATATCAT  | 7620 |
|    | GTAAGTTGCT GATAGGTTTC CAGTTTTCCG CTCCTAGGTC TGCATATTGT ACTTTTCCTC  | 7680 |
|    | TTACTCGACT TAACCAGTAC CAACCCAGCT TCTCAACGGA TTTATACCAT GGCACCTTAA  | 7740 |
| 10 | AGCCAGCATC ACTGACAATG AGCGGTGTGG TGTTACTCGG TAGAATGCTC GCAAGGTCGG  | 7800 |
|    | CTAGAAATTG GTCATGAGCT TTCTTTGAAC ATTGCTCTGA AAGCGGGAAC GCTTTCTCAT  | 7860 |
|    | AAAGAGTAAC AGAACGACCG TGTAGTGC GA CTGAAGCTCG CAATACCATA AGCCGTTTTT | 7920 |
|    | GCTCACGGAT ATCAGACCAG TCAACAAGTA CAATGGGCAT CGTATTGCCC GAACAGATAA  | 7980 |
|    | AGCTAGCATG CCAACGGTAT ACAGCGAGTC GCTCTTTGTG GAGGTGACGA TTACCTAACA  | 8040 |
| 15 | ATCGGTTCGAT TCGTTTGATG TTATGTTTTG TTCTCGCTTT GGTGTCAGG TTACGGCCAA  | 8100 |
|    | GTTTCGGTAAG AGTGAGAGTT TTACAGTCAA GTAAGGCGTG GCAAGCCAAC GTTAAGCTGT | 8160 |
|    | TGAGTCGTTT TAAGTGTAAT TCGGGGCAGA ATTGGTAAAG AGAGTCGTGT AAAATATCGA  | 8220 |
|    | GTTTCGCACAT TTTGTTGTCT GATTATTGAT TTTTGGCGAA ACCATTTGAT CATATGACAA | 8280 |
| 20 | GATGTGTATC TACCTTAACT TAATGATTTT GATAAAAATC ATTAGGGGAT TCATCAGACT  | 8340 |
|    | TACGCATCTT TCATTATGGG AATTAGGTCA GTAATTATGA CAAAAAATTA TGCATTATTA  | 8400 |
|    | TCCGTCTCAG ATAAAACGCA AATCGTTGAA TTTGCCCAAG GTTTGGTAGA ATCTGGCTTT  | 8460 |
|    | GGTATTTTAT CCACAGGTGG TACTTTTAAA CTCTTAAAG AACATGGGAT TGACGCCATT   | 8520 |
|    | GAGGTTTCTG CCCATACAGG TTTTGCTGAA ATGATGGATG GTCGTGTTAA GACCCTACAT  | 8580 |
| 25 | CCCAAATTC ATGGTGGTAT TTTGGGCCGT CGTGGCATTG ATGATGCCAT TATGAATGAA   | 8640 |
|    | CATGGCATTG ATCGCATTGA TATCGTTGTC GTGAATTTAT ATCCATTTGC CAACACGGTC  | 8700 |
|    | GCCAAAGACG GTGTTGTTAT GTCTGATGCG ATTGAAAATA TTGATATTGG TGGGCCTGCT  | 8760 |
|    | ATGGTACGCT CAGCCGCCAA AAATCATGCC CATGTTGGTA TTATCACCAG CCCAAATGAC  | 8820 |
| 30 | TACTCACGCA TCCTAGATGA ACTAAAAAAC CAAGGTCATT TAAGCCACAA CACTCGTTTT  | 8880 |
|    | GATTTGGCAG TCAAAGCATT TGAACACACT GCCGCCTATG ATGGTATGAT TGCCAGCTGG  | 8940 |
|    | CTAGGTGCAC GCTTACCAGT GGATAAAGAG ACGGCACCCA GTGATGATGC CACTGCAACC  | 9000 |
|    | ACTCAATTTT CACGCACTTT TAATCACCAA TTCACCAAAG CACAAGAGCT TAGATATGGC  | 9060 |
|    | GAAAACCCAC ATCAGTCAGC AGCCTTTTAT GTAGATGATC ATGCAACAGA AGCGTCTGTT  | 9120 |
| 35 | GCGACTGCAC AGCAATTACA AGGTAAAGCG TTGTCTTATA ATAATATTGC TGATACCGAT  | 9180 |
|    | GCGGCACTTG AGTGTGTCAA ATCTTTTACC ACGCCTGCTT GTGTGATTGT CAAACATGCC  | 9240 |



AATCCTTGTG GTGTTGCAAC ATCAGAAAAC GGTATTTTAG ATGCTTATCA CTTAGCATAT 9300  
 GCAACCGATC CTGAATCTGC CTTTGGTGGC ATTATTGCCT TTAACCGAGA ATTAGACAGT 9360  
 GATACAGCCC GTACCATCGT TGAGCGTCAA TTTGTTGAAG TCATCATCGC ACCAAGCATC 9420  
 GCTGAAGGTG TTCTAGAGCG GCCGCGGGCC CATCGATTTT CCACCCGGGT GGGGTACCAG 9480  
 5 GTAAGTGTAC CCAATTCGCC CTATAGTGAG TCGTATTACA ATTCAGTGGC CGTCGTTTTA 9540  
 CA 9542

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 2123 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 15 | Met | Asn | His | Ile | Tyr | Lys | Val | Ile | Phe | Asn | Lys | Ala | Thr | Gly | Thr | Phe |
|    | 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
|    | Met | Ala | Val | Ala | Glu | Tyr | Ala | Lys | Ser | His | Ser | Thr | Gly | Gly | Gly | Ser |
|    |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
|    | Cys | Ala | Thr | Gly | Gln | Val | Gly | Ser | Val | Arg | Thr | Leu | Ser | Phe | Ala | Arg |
|    |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
|    | Ile | Ala | Ala | Leu | Ala | Val | Leu | Val | Ile | Gly | Ala | Thr | Leu | Asn | Gly | Ser |
|    |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
|    | Ala | Tyr | Ala | Gly | Ile | Gly | Ile | Ser | Glu | Ala | Asp | Gly | Gly | Lys | Gly | Gly |
|    | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| 20 | Ala | Asn | Ala | Arg | Gly | Asp | Lys | Ser | Ile | Ala | Ile | Gly | Asp | Ile | Ala | Gln |
|    |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
|    | Ala | Leu | Gly | Ser | Gln | Ser | Ile | Ala | Ile | Gly | Asp | Asn | Lys | Ile | Val | His |
|    |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
|    | Asn | Ser | Asn | Asn | Asn | Ala | Asn | Ile | Gly | Ala | Lys | Ala | Ser | Gly | Asn | Glu |
|    |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
|    | Ser | Ile | Ala | Ile | Gly | Gly | Asp | Val | Leu | Ala | Ser | Gly | His | Ala | Ser | Ile |
|    |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| 25 | Ala | Ile | Gly | Ser | Asp | Asp | Leu | Tyr | Leu | Lys | Lys | Glu | Thr | Val | Gln | Gln |
|    | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
|    | Ile | Ser | Glu | Leu | Leu | Pro | Ile | Ile | Arg | Gly | Gln | Lys | Ala | Leu | Asn | Asp |
|    |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
|    | Ile | Tyr | Gln | Leu | Ala | Asp | Thr | Asn | Leu | Gln | Lys | Tyr | Arg | Arg | Thr | His |
|    |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
|    | Ala | Gln | Gly | His | Ala | Ser | Thr | Ala | Val | Gly | Ala | Met | Ser | Tyr | Ala | Lys |
|    |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
|    | Gly | His | Phe | Ser | Asn | Ala | Phe | Gly | Thr | Arg | Ala | Thr | Ala | Glu | Gly | Thr |
|    |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| 30 | Tyr | Ser | Leu | Ala | Val | Gly | Leu | Thr | Ala | Thr | Ala | Lys | Ala | Ala | Ser | Ser |
|    | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
|    | Ile | Ala | Val | Gly | Ser | Asn | Ala | Gln | Ala | Ile | Gly | Phe | Ala | Ala | Thr | Ala |
|    |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
|    | Val | Gly | Gly | Ser | Thr | Gln | Val | Asn | Leu | Asn | Arg | Gly | Ile | Ala | Leu | Gly |
|    |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
|    | Phe | Gly | Ser | Gln | Val | Leu | Gln | Lys | Asp | Asn | Asp | Val | Asn | Ala | Ala | Asn |
|    |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| 35 | Val | Arg | Ala | Tyr | Ala | Pro | Asp | Asp | Asn | Gln | Pro | Ile | Asp | Asn | Arg | Tyr |
|    |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |     |
|    | Lys | Ala | Thr | Phe | Lys | Asn | Gly | Ala | Thr | Asp | Val | Phe | Ser | Ile | Gly | Asn |
|    |     | 305 |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
|    | Ser | Asn | Gly | Asn | Asp | Ser | Ile | Arg | Arg | Lys | Ile | Ile | Asn | Val | Gly | Ala |

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|    |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
|    | Gly | Ser | Ala | Asp | Thr | Asp | Ala | Val | Asn | Val | Ala | Gln | Leu | Lys | Glu | Ala |
|    |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
|    | Val | Arg | Leu | Ala | Asn | Arg | Gln | Ile | Thr | Phe | Lys | Gly | Asp | Asp | Ser | Asn |
|    |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
|    | Asn | Arg | Val | Glu | Lys | Gly | Leu | Gly | Lys | Thr | Leu | Thr | Ile | Thr | Gly | Gly |
|    |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| 5  | Ala | Gln | Thr | Ser | Ala | Leu | Thr | Asp | His | Asn | Ile | Gly | Val | Val | Gln | Asn |
|    | 385 |     |     |     |     |     | 390 |     |     |     | 395 |     |     |     | 400 |     |
|    | Gly | Asp | Gly | Leu | Lys | Val | Gln | Leu | Ala | Glu | Thr | Leu | Thr | Ser | Leu | Lys |
|    |     |     |     |     | 405 |     |     |     |     | 410 |     |     |     | 415 |     |     |
|    | Met | Val | Thr | Thr | Glu | Asn | Leu | Thr | Ala | Asn | Glu | Lys | Val | Thr | Val | Gly |
|    |     |     |     |     | 420 |     |     |     | 425 |     |     |     |     | 430 |     |     |
|    | Lys | Thr | Arg | Leu | Thr | Thr | Asp | Lys | Ile | Gly | Phe | Thr | Asn | Asp | Met | Asn |
|    |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
|    | Gly | Ile | Asp | Glu | Ser | Lys | Pro | Tyr | Leu | Asp | Lys | Asp | Thr | Gly | Ile | His |
|    |     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| 10 | Ala | Gly | Gly | Gln | Lys | Ile | Thr | Lys | Leu | Thr | Ala | Gly | Val | Val | Asp | Asp |
|    | 465 |     |     |     |     |     | 470 |     |     |     | 475 |     |     |     | 480 |     |
|    | Asp | Ala | Ala | Thr | Tyr | Gly | Gln | Leu | Lys | Lys | Val | Asn | Gln | Thr | Ala | Glu |
|    |     |     |     |     | 485 |     |     |     |     | 490 |     |     |     | 495 |     |     |
|    | Ser | Ala | Leu | Gln | Thr | Phe | Thr | Val | Lys | Val | Asp | Lys | Asn | Gly | Asn |     |
|    |     |     | 500 |     |     |     |     |     | 505 |     |     |     | 510 |     |     |     |
|    | Asp | Ala | Asn | Asp | Ser | Lys | Ile | Ile | Thr | Val | Gly | Lys | Asn | Asn | Lys | Pro |
|    |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| 15 | Asp | Gly | Thr | Gln | Val | Asn | Thr | Leu | Lys | Leu | Lys | Gly | Glu | Asn | Gly | Val |
|    |     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
|    | Asp | Val | Thr | Thr | Glu | Thr | Asn | Gly | Thr | Val | Thr | Phe | Gly | Leu | Asn | Gln |
|    | 545 |     |     |     |     |     | 550 |     |     |     | 555 |     |     |     | 560 |     |
|    | Asn | Asn | Gly | Leu | Thr | Val | Gly | Asn | Ser | Thr | Leu | Asn | Asn | Asp | Gly | Leu |
|    |     |     |     |     | 565 |     |     |     |     | 570 |     |     |     | 575 |     |     |
|    | Ser | Val | Lys | Asn | Thr | Asn | Ser | Asn | Lys | Gln | Ile | Gln | Val | Gly | Ala | Asp |
|    |     |     | 580 |     |     |     |     |     | 585 |     |     |     | 590 |     |     |     |
|    | Gly | Ile | Thr | Phe | Thr | Asp | Ile | Ser | Asn | Ser | Lys | Pro | Gly | Ala | Gly | Ile |
|    |     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| 20 | Glu | Asn | Thr | Thr | Arg | Ile | Thr | Arg | Asp | Gly | Ile | Gly | Phe | Ala | Asn | Asn |
|    |     |     | 610 |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
|    | Thr | Gly | Ser | Leu | Asp | Ala | Asn | Lys | Pro | Arg | Leu | Thr | Pro | Thr | Gly | Ile |
|    |     |     |     |     | 630 |     |     |     |     |     | 635 |     |     |     | 640 |     |
|    | Asn | Ala | Gly | Gly | Lys | Glu | Leu | Thr | Asn | Val | Gln | Ser | Ala | Ile | Asn | Pro |
|    |     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
|    | Ala | Thr | Asn | Gly | Gly | Gln | Leu | Asp | Phe | Met | Asn | Arg | Leu | Ser | Thr | Ala |
|    |     |     | 660 |     |     |     |     |     | 665 |     |     |     | 670 |     |     |     |
| 25 | Asn | Thr | Glu | Lys | Ser | Gly | Ser | Ala | Ala | Thr | Ile | Lys | Asp | Leu | Tyr | Asn |
|    |     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |
|    | Leu | Ser | Gln | Val | Pro | Leu | Thr | Phe | Ala | Gly | Asp | Thr | Gly | Pro | Asn | Val |
|    |     |     | 690 |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |
|    | Thr | Lys | Lys | Leu | Gly | Glu | Ile | Leu | Lys | Val | Lys | Gly | Gly | Lys | Thr | Thr |
|    |     |     | 705 |     |     | 710 |     |     |     |     | 715 |     |     |     | 720 |     |
|    | Ala | Asp | Asp | Leu | Thr | Lys | Asn | Asn | Ile | Gly | Val | Val | Ala | Asp | Ser | Thr |
|    |     |     |     |     | 725 |     |     |     |     | 730 |     |     |     | 735 |     |     |
|    | Asp | Asn | Ser | Leu | Thr | Val | Lys | Leu | Ala | Lys | Thr | Leu | Ser | Asp | Leu | Asp |
|    |     |     | 740 |     |     |     |     |     | 745 |     |     |     | 750 |     |     |     |
| 30 | Ala | Val | Asn | Thr | Lys | Thr | Leu | Thr | Ala | Ser | Asp | Lys | Val | Thr | Val | Asp |
|    |     |     | 755 |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
|    | Ser | Gly | Asn | Asn | Thr | Ala | Lys | Leu | Gln | Asn | Gly | Asp | Leu | Thr | Phe | Ser |
|    |     |     | 770 |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |
|    | Lys | Gln | Asn | Thr | Gly | Ala | Thr | Pro | Ala | Thr | Asn | Ser | Lys | Thr | Ile | Tyr |
|    |     |     | 785 |     |     | 790 |     |     |     |     | 795 |     |     |     | 800 |     |
|    | Gly | Val | Asp | Gly | Leu | Lys | Phe | Thr | Asp | Asn | Asn | Gly | Ile | Ala | Leu | Asp |
|    |     |     |     |     | 805 |     |     |     |     | 810 |     |     |     | 815 |     |     |
| 35 | Gly | Thr | Thr | Tyr | Ile | Thr | Lys | Asp | Lys | Val | Gly | Phe | Ala | Lys | Gln | Asp |
|    |     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |
|    | Gly | Ser | Leu | Asp | Lys | Ser | Lys | Pro | Tyr | Leu | Asp | Lys | Asp | Lys | Leu | Lys |
|    |     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |
|    | Val | Gly | Glu | Val | Glu | Ile | Thr | Thr | Asn | Gly | Ile | Asn | Ala | Gly | Gly | Lys |

|    |   |      |     |      |      |
|----|---|------|-----|------|------|
|    | 850   |      | 855 |      | 860  |
|    | Ala Ile Thr Gly Leu Ser Asn Thr Leu Thr Asp Ala Thr Asn Ala Thr |      |     |      |      |
|    | 865   |      | 870 |      | 875  |
|    | Thr Gly His Val Thr Gln Leu Gly Ile Val Asp Ser Thr Asp Lys Thr |      |     |      | 880  |
|    |   | 885  |     | 890  |      |
|    | Arg Ala Ala Ser Ile Gly Asp Val Leu Asn Ala Gly Phe Asn Leu Lys |      |     |      | 895  |
|    |   | 900  |     | 905  |      |
| 5  | Asn Asn Gly Asp Ala Lys Asp Phe Val Ser Thr Tyr Asp Thr Val Asp |      |     |      | 910  |
|    |   | 915  |     | 920  |      |
|    | Phe Ile Asn Gly Asn Ala Thr Thr Ala Lys Val Thr Tyr Asp Gly Lys |      |     |      | 925  |
|    |   | 930  |     | 935  |      |
|    | Ala Ser Lys Val Ala Tyr Asp Val Asn Val Asp Gly Thr Thr Ile His |      |     |      | 940  |
|    |   | 945  |     | 950  |      |
|    | Leu Thr Gly Ala Asp Gly Asn Lys Asn Gln Ile Gly Val Lys Thr Thr |      |     |      | 955  |
|    |   | 965  |     | 970  |      |
|    | Thr Leu Thr Lys Thr Asp Ala Lys Gly Asp Lys Ala Ile Asn Phe Ser |      |     |      | 975  |
|    |   | 980  |     | 985  |      |
| 10 | Val Asn Ser Gly Asp Asp Lys Ala Leu Ile Asn Ala Lys Asp Ile Ala |      |     |      | 990  |
|    |   | 995  |     | 1000 |      |
|    | Asp Asn Leu Asn Thr Leu Ala Gly Glu Ile Arg Asn Thr Lys Gly Thr |      |     |      | 1005 |
|    |   | 1010 |     | 1015 |      |
|    | Ala Asp Thr Ala Leu Gln Thr Phe Gln Val Lys Lys Val Lys Glu Asn |      |     |      | 1020 |
|    |   | 1025 |     | 1030 |      |
|    | Gly Asp Asp Asp Asn Asp Ala Asp Thr Ile Thr Val Gly Lys Asp Ala |      |     |      | 1035 |
|    |   | 1045 |     | 1050 |      |
| 15 | Lys Thr Asn Gln Val Asn Thr Leu Lys Leu Lys Gly Lys Asn Gly Leu |      |     |      | 1055 |
|    |   | 1060 |     | 1065 |      |
|    | Asp Ile Gln Thr Asn Lys Asp Gly Thr Val Thr Phe Gly Ile Asn Thr |      |     |      | 1070 |
|    |   | 1075 |     | 1080 |      |
|    | Gln Ser Gly Leu Lys Ala Gly Asn Asn Thr Thr Leu Asn Asn Asn Gly |      |     |      | 1085 |
|    |   | 1090 |     | 1095 |      |
|    | Leu Ser Ile Lys Asn Thr Ala Gly Asn Glu Gln Ile Gln Val Gly Ala |      |     |      | 1100 |
|    |   | 1105 |     | 1110 |      |
|    | Asp Gly Val Lys Phe Ala Lys Val Asn Asn Gly Val Val Gly Ala Gly |      |     |      | 1115 |
|    |   | 1125 |     | 1130 |      |
| 20 | Ile Asp Gly Thr Thr Arg Ile Thr Arg Asp Glu Ile Gly Phe Ala Gly |      |     |      | 1135 |
|    |   | 1140 |     | 1145 |      |
|    | Thr Asn Gly Ser Leu Asp Lys Ser Lys Pro His Leu Ser Lys Asp Gly |      |     |      | 1150 |
|    |   | 1155 |     | 1160 |      |
|    | Ile Asn Ala Gly Gly Lys Lys Ile Thr Asn Ile Gln Ser Gly Glu Ile |      |     |      | 1165 |
|    |   | 1170 |     | 1175 |      |
|    | Ala Gln Asn Ser Asn Asp Ala Val Thr Gly Gly Lys Ile Tyr Asp Leu |      |     |      | 1180 |
|    |   | 1185 |     | 1190 |      |
| 25 | Lys Thr Glu Leu Glu Asn Lys Ile Ser Ser Thr Ala Lys Thr Ala Gln |      |     |      | 1195 |
|    |   | 1205 |     | 1210 |      |
|    | Asn Ser Leu His Glu Phe Ser Val Ala Asp Glu Gln Gly Asn Asn Phe |      |     |      | 1215 |
|    |   | 1220 |     | 1225 |      |
|    | Thr Val Ser Asn Pro Tyr Ser Ser Tyr Asp Thr Ser Lys Thr Ser Asp |      |     |      | 1230 |
|    |   | 1235 |     | 1240 |      |
|    | Val Ile Thr Phe Ala Gly Glu Asn Gly Ile Thr Thr Lys Val Asn Lys |      |     |      | 1245 |
|    |   | 1250 |     | 1255 |      |
|    | Gly Val Val Arg Val Gly Ile Asp Gln Thr Lys Gly Leu Thr Thr Pro |      |     |      | 1260 |
|    |   | 1265 |     | 1270 |      |
| 30 | Lys Leu Thr Val Gly Asn Asn Asn Gly Lys Gly Ile Val Ile Asp Ser |      |     |      | 1275 |
|    |   | 1285 |     | 1290 |      |
|    | Gln Asn Gly Gln Asn Thr Ile Thr Gly Leu Ser Asn Thr Leu Ala Asn |      |     |      | 1295 |
|    |   | 1300 |     | 1305 |      |
|    | Val Thr Asn Asp Lys Gly Ser Val Arg Thr Thr Glu Gln Gly Lys Ile |      |     |      | 1310 |
|    |   | 1315 |     | 1320 |      |
|    | Ile Lys Asp Glu Asp Lys Thr Arg Ala Ala Ser Ile Val Asp Val Leu |      |     |      | 1325 |
|    |   | 1330 |     | 1335 |      |
| 35 | Ser Ala Gly Phe Asn Leu Gln Gly Asn Gly Glu Ala Val Asp Phe Val |      |     |      | 1340 |
|    |   | 1345 |     | 1350 |      |
|    | Ser Thr Tyr Asp Thr Val Asn Phe Ala Asp Gly Asn Ala Thr Thr Ala |      |     |      | 1355 |
|    |   | 1365 |     | 1370 |      |
|    | Lys Val Thr Tyr Asp Asp Thr Ser Lys Thr Ser Lys Val Val Tyr Asp |      |     |      | 1375 |

1380 1385 1390  
 Val Asn Val Asp Asp Thr Thr Ile Glu Val Lys Asp Lys Lys Leu Gly  
 1395 1400 1405  
 Val Lys Thr Thr Thr Leu Thr Ser Thr Gly Thr Gly Ala Asn Lys Phe  
 1410 1415 1420  
 Ala Leu Ser Asn Gln Ala Thr Gly Asp Ala Leu Val Lys Ala Ser Asp  
 425 1430 1435 1440  
 5 Ile Val Ala His Leu Asn Thr Leu Ser Gly Asp Ile Gln Thr Ala Lys  
 1445 1450 1455  
 Gly Ala Ser Gln Ala Asn Ser Ser Ala Gly Tyr Val Asp Ala Asp Gly  
 1460 1465 1470  
 Asn Lys Val Ile Tyr Asp Ser Thr Asp Asn Lys Tyr Tyr Gln Ala Lys  
 1475 1480 1485  
 Asn Asp Gly Thr Val Asp Lys Thr Lys Glu Val Ala Lys Asp Lys Leu  
 1490 1495 1500  
 Val Ala Gln Ala Gln Thr Pro Asp Gly Thr Leu Ala Gln Met Asn Val  
 505 1510 1515 1520  
 10 Lys Ser Val Ile Asn Lys Glu Gln Val Asn Asp Ala Asn Lys Lys Gln  
 1525 1530 1535  
 Gly Ile Asn Glu Asp Asn Ala Phe Val Lys Gly Leu Glu Lys Ala Ala  
 1540 1545 1550  
 Ser Asp Asn Lys Thr Lys Asn Ala Ala Val Thr Val Gly Asp Leu Asn  
 1555 1560 1565  
 Ala Val Ala Gln Thr Pro Leu Thr Phe Ala Gly Asp Thr Gly Thr Thr  
 1570 1575 1580  
 15 Ala Lys Lys Leu Gly Glu Thr Leu Thr Ile Lys Gly Gly Gln Thr Asp  
 585 1590 1595 1600  
 Thr Asn Lys Leu Thr Asp Asn Asn Ile Gly Val Val Ala Gly Thr Asp  
 1605 1610 1615  
 Gly Phe Thr Val Lys Leu Ala Lys Asp Leu Thr Asn Leu Asn Ser Val  
 1620 1625 1630  
 Asn Ala Gly Gly Thr Lys Ile Asp Asp Lys Gly Val Ser Phe Val Asp  
 1635 1640 1645  
 Ser Ser Gly Gln Ala Lys Ala Asn Thr Pro Val Leu Ser Ala Asn Gly  
 1650 1655 1660  
 20 Leu Asp Leu Gly Gly Lys Val Ile Ser Asn Val Gly Lys Gly Thr Lys  
 665 1670 1675 1680  
 Asp Thr Asp Ala Ala Asn Val Gln Gln Leu Asn Glu Val Arg Asn Leu  
 1685 1690 1695  
 Leu Gly Leu Gly Asn Ala Gly Asn Asp Asn Ala Asp Gly Asn Gln Val  
 1700 1705 1710  
 Asn Ile Ala Asp Ile Lys Lys Asp Pro Asn Ser Gly Ser Ser Ser Asn  
 1715 1720 1725  
 25 Arg Thr Val Ile Lys Ala Gly Thr Val Leu Gly Gly Lys Gly Asn Asn  
 1730 1735 1740  
 Asp Thr Glu Lys Leu Ala Thr Gly Gly Val Gln Val Gly Val Asp Lys  
 745 1750 1755 1760  
 Asp Gly Asn Ala Asn Gly Asp Leu Ser Asn Val Trp Val Lys Thr Gln  
 1765 1770 1775  
 Lys Asp Gly Ser Lys Lys Ala Leu Leu Ala Thr Tyr Asn Ala Ala Gly  
 1780 1785 1790  
 Gln Thr Asn Tyr Leu Thr Asn Asn Pro Ala Glu Ala Ile Asp Arg Ile  
 1795 1800 1805  
 30 Asn Glu Gln Gly Ile Arg Phe Phe His Val Asn Asp Gly Asn Gln Glu  
 1810 1815 1820  
 Pro Val Val Gln Gly Arg Asn Gly Ile Asp Ser Ser Ala Ser Gly Lys  
 825 1830 1835 1840  
 His Ser Val Ala Ile Gly Phe Gln Ala Lys Ala Asp Gly Glu Ala Ala  
 1845 1850 1855  
 Val Ala Ile Gly Arg Gln Thr Gln Ala Gly Asn Gln Ser Ile Ala Ile  
 1860 1865 1870  
 35 Gly Asp Asn Ala Gln Ala Thr Gly Asp Gln Ser Ile Ala Ile Gly Thr  
 1875 1880 1885  
 Gly Asn Val Val Ala Gly Lys His Ser Gly Ala Ile Gly Asp Pro Ser  
 1890 1895 1900  
 Thr Val Lys Ala Asp Asn Ser Tyr Ser Val Gly Asn Asn Asn Gln Phe



Ser Gln Ser Ile Ala Ile Gly Asp  
 35 40

(2) INFORMATION FOR SEQ ID NO:13:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser  
 1 5 10 15  
 Ile Ala Ile Gly Asp Ile Ala Gln  
 20

(2) INFORMATION FOR SEQ ID NO:14:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20 Gly Ala Arg Gly Cys Asn Gly Ala Tyr Gly Gly Asn Gly Gly Asn Ala  
 1 5 10 15  
 Ala Arg

(2) INFORMATION FOR SEQ ID NO:15:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

30 Tyr Thr Gly Asn Gly Cys Asp Ala Thr Arg Thr Cys Asn Cys Cys Asp  
 1 5 10 15  
 Ala Thr

(2) INFORMATION FOR SEQ ID NO:16:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAAGCGGACG GGGGAAA

18

(2) INFORMATION FOR SEQ ID NO:17:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 TTGCGCAATG TCACCAAT

18

(2) INFORMATION FOR SEQ ID NO:18:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAAGCGGACG GGGGGAAAGG CGGAGCCAAT GCGCGCGGTG ATAAATCCAT TGCTATTGGT

60

20 GACATTGCGC AA

72

(2) INFORMATION FOR SEQ ID NO:19:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser  
1 5 10 15

30 Ile Ala Ile Gly Asp Ile Ala Gln  
20

35